



SEQUENCE LISTING

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<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
OF TREATMENT THEREWITH

<130> 08702.0081-01000

<140> 09/627,896

<141> 2000-07-27

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 405

<212> DNA

<213> Murine sp.

<220>

<221> CDS

<222> (1)..(405)

<223> Anti-B7-2 heavy chain

<400> 1

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Met	Gly	Trp	Asn	Cys	Ile	Ile	Phe	Phe	Leu	Val	Thr	Thr	Ala	Thr	Gly	
1				5					10					15		

gtg	cac	tcc	cag	gtc	cag	ctg	cag	cag	tct	ggg	cct	gag	ctg	gtg	agg	96
Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Arg	
			20					25						30		

cct	ggg	gaa	tca	gtg	aag	att	tcc	tgc	aag	ggt	tcc	ggc	tac	aca	ttc	144
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe	
			35					40					45			

act	gat	tat	gct	ata	cag	tgg	gtg	aag	cag	agt	cat	gca	aag	agt	cta	192
Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Lys	Gln	Ser	His	Ala	Lys	Ser	Leu	

50

55

60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac 240
 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
 65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc 288
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
 85 90 95

aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc 336
 Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile
 100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga 384
 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
 115 120 125

acc tca gtc acc gtc tcc tca 405
 Thr Ser Val Thr Val Ser Ser
 130 135

<210> 2

<211> 135

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 heavy chain

<400> 2

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly
 1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg
 20 25 30

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu
 50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile

100

105

110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
 115 120 125

Thr Ser Val Thr Val Ser Ser
 130 135

<210> 3

<211> 396

<212> DNA

<213> Murine sp.

<220>

<221> CDS

<222> (1)..(396)

<223> Anti-B7-2 light chain

<400> 3

atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct 48
 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser
 1 5 10 15

ggt acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct 96
 Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala
 20 25 30

gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt 144
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
 35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag 192
 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg 240
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat 288
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 85 90 95

ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat 336
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
 100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag 384
 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
 115 120 125

ctg gaa ata aaa
Leu Glu Ile Lys
130

396

<210> 4
<211> 132
<212> PRT
<213> Murine sp.

<220>
<223> Anti-B7-2 light chain

<400> 4
Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala
20 25 30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125
Leu Glu Ile Lys
130

<210> 5
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(405)

<400> 5

atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca gct aca ggt	48
Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly	
1 5 10 15	
gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc	144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc	192
Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50 55 60	
gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac	240
Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn	
65 70 75 80	
cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc	288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser	
85 90 95	
aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt	384
Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly	
115 120 125	
acc ctt gtc acc gtc tcc tca	405
Thr Leu Val Thr Val Ser Ser	
130 135	

<210> 6

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 heavy chain

<400> 6

Met	Gly	Trp	Asn	Cys	Ile	Ile	Phe	Phe	Leu	Val	Thr	Thr	Ala	Thr	Gly		
1				5					10					15			
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys		
			20					25					30				
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe		
		35					40					45					
Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu		
	50					55					60						
Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn		
65					70					75					80		
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Thr	Ser		
				85					90					95			
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val		
			100					105						110			
Tyr	Tyr	Cys	Ala	Arg	Ala	Ala	Trp	Tyr	Met	Asp	Tyr	Trp	Gly	Gln	Gly		
		115					120					125					
Thr	Leu	Val	Thr	Val	Ser	Ser											
	130					135											

<210> 7

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(396)

<400> 7

atg	gat	tca	cag	gcc	cag	gtt	ctt	ata	ttg	ctg	ctg	cta	tgg	gta	tct		48
Met	Asp	Ser	Gln	Ala	Gln	Val	Leu	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser		
1				5				10					15				
ggc	acc	tgt	ggg	gac	att	gtg	ctg	aca	cag	tct	cca	gat	tcc	ctg	gct		96
Gly	Thr	Cys	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala		
			20					25					30				

gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt	144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser	
35 40 45	

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag	192
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln	
50 55 60	

aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg	240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg	
65 70 75 80	

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat	288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
85 90 95	

ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat	336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr	
100 105 110	

tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag	384
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys	
115 120 125	

gtg gaa ata aaa	396
Val Glu Ile Lys	
130	

<210> 8
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Humanized
 murine anti-human B7-2 light chain

<400> 8
Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser
1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys
130

<210> 9
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR1 of
humanized murine anti-human B7-2 heavy chain

<220>
<221> CDS
<222> (1)..(15)

<400> 9
gat tat gct ata cag
Asp Tyr Ala Ile Gln
1 5

15

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR1 of humanized
murine anti-human B7-2 heavy chain

<400> 10
Asp Tyr Ala Ile Gln
1 5

<210> 11

<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR2 of
humanized murine anti-human B7-2 heavy chain

<220>
<221> CDS
<222> (1)..(51)

<400> 11
gtt att aat att tac tat gat aat aca aac tac aac cag aag ttt aag 48
Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

ggc 51
Gly

<210> 12
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR2 of humanized
murine anti-human B7-2 heavy chain

<400> 12
Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR3 of
humanized murine anti-human B7-2 heavy chain

<220>
<221> CDS
<222> (1)..(21)

<400> 13

gcg gcc tgg tat atg gac tac
Ala Ala Trp Tyr Met Asp Tyr
1 5

21

<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR3 of humanized
murine anti-human B7-2 heavy chain

<400> 14
Ala Ala Trp Tyr Met Asp Tyr
1 5

<210> 15
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR1 of
humanized murine anti-human B7-2 light chain

<220>
<221> CDS
<222> (1)..(51)

<400> 15
aaa tcc agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg 48
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu
1 5 10 15

gct 51
Ala

<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR1 of humanized
murine anti-human B7-2 light chain

<400> 16

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu
1 5 10 15

Ala

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR2 of
humanized murine anti-human B7-2 light chain

<220>
<221> CDS
<222> (1)..(21)

<400> 17
tgg gca tcc act agg gaa tct
Trp Ala Ser Thr Arg Glu Ser
1 5

21

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR2 of humanized
murine anti-human B7-2 light chain

<400> 18
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR3 of
humanized murine anti-human B7-2 light chain

<220>
<221> CDS
<222> (1)..(24)

<400> 19

acg caa tct tat aat ctt tac acg

24

Thr Gln Ser Tyr Asn Leu Tyr Thr

1

5

<210> 20

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of humanized
murine anti-human B7-2 light chain

<400> 20

Thr Gln Ser Tyr Asn Leu Tyr Thr

1

5

<210> 21

<211> 1960

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (12)..(408)

<220>

<221> CDS

<222> (768)..(1087)

<400> 21

tctagaccac c atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta 50

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu

1

5

10

tgg gta tct ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat 98

Trp Val Ser Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp

15

20

25

tcc ctg gct gta agc tta gga gag agg gcc act att agc tgc aaa tcc 146

Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser

30

35

40

45

agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg 194

Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp

50

55

60

tac cag cag aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca	242
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala	
65 70 75	
tcc act agg gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct	290
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser	
80 85 90	
ggg aca gat ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg	338
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val	
95 100 105	
gca gtt tat tac tgc agc caa tct tat aat ctt tac acg ttc gga cag	386
Ala Val Tyr Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln	
110 115 120 125	
ggg acc aag gtg gaa ata aaa c gtaagtagtc ttctcaactc tagaaattct	438
Gly Thr Lys Val Glu Ile Lys	
130	
aaactctgag ggggtcggat gacgtggcca ttctttgcct aaagcattga gtttactgca	498
aggtcagaaa agcatgcaaa gccctcagaa tggctgcaaa gagctccaac aaaacaattt	558
agaactttat taaggaatag ggggaagcta ggaagaaact caaaacatca agattttaaa	618
tacgcttctt ggtctccttg ctataattat ctgggataag catgctgttt tctgtctgtc	678
cctaacatgc cctgtgatta tccgcaaaca acacacccaa gggcagaact ttgttactta	738
aacaccatcc tgtttgcttc tttcctcag ga act gtg gct gca cca tct gtc	790
Arg Thr Val Ala Ala Pro Ser Val	
135 140	
ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct	838
Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser	
145 150 155	
gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag	886
Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln	
160 165 170	
tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc	934
Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val	
175 180 185	
aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg	982
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu	
190 195 200	
acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa	1030

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 205 210 215 220

gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg 1078
 Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 225 230 235

gga gag tgt tagaggaga agtgcccca cctgctcctc agttccagcc 1127
 Gly Glu Cys

tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc 1187

ggctcctccag ctcatactttc acctcacccc cctcctcctc cttggcttta attatgctaa 1247

tgttggagga gaatgaataa ataaagtga tctttgcacc tgtggtttct ctctttcctc 1307

atttaataat tattatctgt tgttttacca actactcaat ttctcttata agggactaaa 1367

tatgtagtca tctaaggcg cataaccatt tataaaaatc atccttcatt ctattttacc 1427

ctatcatcct ctgcaagaca gtccctcctc aaaccacaa gccttctgtc ctcacagtcc 1487

cctgggccat ggtaggagag acttgcttcc ttgttttccc ctcctcagca agccctcata 1547

gtccttttta agggtgacag gtcttacagt catatatcct ttgattcaat tccctgggaa 1607

tcaaccaaag caaatTTTTTc aaaagaagaa acctgctata aagagaatca ttcattgcaa 1667

catgatataa aataacaaca caataaaagc aattaaataa acaaacaata gggaaatggt 1727

taagttcatc atggtactta gacttaatgg aatgtcatgc cttatttaca tttttaaaca 1787

ggtagtgagg gactcctgtc tgccaagggc cgtattgagt actttccaca acctaatTTa 1847

atccacacta tactgtgaga ttaaaaacat tcattaaaat gttgcaaagg ttctataaag 1907

ctgagagaca aatatattct ataactcagc aatcccactt ctaggatcaa ttc 1960

<210> 22
 <211> 239
 <212> PRT
 <213> Mus sp.

<400> 22
 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser
 1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser
		35					40					45			
Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln
	50					55					60				
Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
	65				70					75					80
Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
				85					90					95	
Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr
			100					105					110		
Tyr	Cys	Ser	Gln	Ser	Tyr	Asn	Leu	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		115					120					125			
Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	130					135					140				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
	145				150					155					160
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
			165						170					175	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			180					185					190		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		195					200					205			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	210					215					220				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
	225				230					235					

<210> 23
 <211> 2249
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (12)..(417)

<220>

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<222> (655)..(948)

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Ala	Thr	Gly	Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	
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Tyr	Thr	Phe	Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	
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Gln	Gly	Leu	Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	
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Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Lys	
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Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ala	Ala	Trp	Tyr	Met	Asp	Tyr	Trp	
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 Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val
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 Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
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 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
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 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
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 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
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 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
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Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	145	150	155	160
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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	195	200	205	
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Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	225	230	235	240
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Ala	Ala	Ala	Pro	Ser	Val	Phe	Leu	245	250		255
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	260	265		270
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Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	355	360		365
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Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	405	410		415

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Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460
